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STUDIES OF THE OUTER MEMBRANE PROTEINS OF CAMPYLOBACTER JEJUNI FOR VACCINE DEVELOPMENT

MIDTERM REPORT

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FOREWORD

The investigator(s) have abided by the National Institutes of Health Guidelines for Research Involving Recombinant DNA Molecules (April 1982) and the Administrative Practices Supplements.



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A. Progress

1. Studies of erythromycin-resistance in Campylobacters.

In collaboration with colleagues at the University of Washington in Seattle, and AFRIMS in Bangkok, we participated in studies to define frequency and mechanism of erythromycinresistance in Campylobacter isolates. Forty-two erythromycin resistant (EmR) strains of Campylobacter from domestic- and foreignacquired human infections, AIDS patients and poultry were examined. Two naturally occurring resistance patterns were found: (1) high resistance to erythromycin, tylosin, clindamycin and vernamycin B (N=41) and (2) resistance to erythromycin and vernamycin B, but not tylosin or clindamycin (N=1). The predominant phenotypic pattern suggested the presence of an rRNA methylase; however, DNA probes to common bacterial genes encoding erythromycin resistance did not hybridize with the EmR Campylobacter, suggesting a novel resistance determinant. Erythromycin-resistant isolates were selected by serial pasage on erythromycin containing media from two erythromycin-sensitive strains (related by plasmid profiles and serotype to naturally occurring EmR strains); however, the pattern and magnitude of resistance in the in vitro isolates was different from the in vivo resistant isolates. Examination of 660 isolates collected in King County, Washington, revealed that ${\tt EmR}\ {\tt C}.$ jejuni were not a substantial problem in human or poultry isolates (0% and 2%) but that EmR C. coli represented 12% and 30% of human and poultry isolates, respectively.

C. coli is a much more significant problem in developing countries, where U.S. troops may be exposed. Previous studies from AFRIMS in Bangkok indicate that the C. coli strains isolated from Thailand are often erythromycin-resistant. High frequency resistance and emergence of resistance to new agents supports the concept that vaccination of troops against campylobacters will be an important preventive measure.

2. The role of Cholera-like Enterotoxin in Campylobacter Enteritis in Thailand.

Although Campylobacter enteritis is usually an inflammatory process in developed countries, watery diarrhea is common in the developing world. Some investigators have found strains of Campylobacter that produce a cholera-like toxin which may be responsible for watery diarrhea. We investigated by ELISA the immune response to cholera toxin and to surface exposed antigens of C. jejuni in children with acute diarrhea in Bangkok. Sera from children infected with Campylobacter (n=29, mean age 13.5 mo) and infected with Shigella (n=26, mean age 23.1 mo) were collected during the acute phase, and 2 and 4 weeks after the diarrheal episode. By

ELISA, children infected with Campylobacter but not Shigella showed a significant increase of antibody levels to C. je juni specific antigens in all three immunoglobulin classes (p<0.01). In the Campylobacter infected group antibody levels were similar whether watery or bloody diarrhea was present, however, children with diarrhea for more than 72h or older than two years of age were less reactive to C. jejuni antigens. Neither Campylobacter- nor Shigella-infected children showed any increase in antibody levels to cholera toxin. Furthermore, 29 Campylobacter isolates from this study did not hybridize with LT or Shiga-like I or II probes. In total, these data argue against a role for enterotoxin in the pathogenesis of Campylobacter enteritis in developing countries. This represents our third study that has indicated that enterotoxins are not important in the pathogenesis of Campylobacter diarrhea. Taken together with negative studies by other investigators, this study indicates that it is no longer worthwhile to pursue enterotoxin as a vaccine component.

3. Investigation of an outbreak of Campylobacter jejuni in Multiple Oklahoma Prisons.

An outbreak of 104 cases of Campylobacter jejuni gastroenteritis occurred in 1988 in four Oklahoma prisons. Cases were defined as persons with diarrhea and three or more other symptoms. hundred inmates (97%) had diarrhea, 69 (67%) had fever, and 24/114 (20%) had positive stool cultures. Case-control studies showed that consumption of pasteurized milk from the prison dairy farm was associated with illness; 90 (87%) cases consumed milk, while only 64 (60%) controls consumed milk (Odds ratio OR = 2.4, p<.05). Manure samples of cattle from the prison dairy farm grew C. je juni strains antigenically similar (Penner 8, 1W; Lior 2) to the human isolates. We performed serologic testing of samples provided from culture-positive, culture-negative (clinical) cases and from unaffected controls using an ELISA based on C. je juni antigens. The culture-positive and clinical cases were more likely to have positive serologic ELISA tests for C. jejuni specific immunoglobulin (p<.0001 for IgA, p<.01 for IgG, and p<.01 for IgM) than the controls. Although a deficit in the pasteurization process was not identified, the milk had elevated coliform counts from samples taken on the day the implicated milk was distributed to the prisons. The results of these findings, implicating pasteurized milk as a vehicle of spread, underscore the importance of proper pasteurization techniques and other proper food handling procedures. This outbreak investigation also points to the utility of serologic tests for diagnosing Campylobacter infection, which could be useful in field settings.

 Identification, purification, and characterization of major antigenic proteins of Campylobacter jejumi.

Our studies of the surface proteins of *C. fetus* and *H. pylori* have indicated that a group of proteins external to the outer membrane are important antigens and provide significant functions for these bacteria. From our previous work, we have identified 4 proteins in the acid-extract from *C. je juni* which may be vaccine candidates. These are PEB1 (migrates at 28 kDa), PEB2 (29kDa) PEB3 (30 kDa), PEB4 (31kDa). In this work, we have developed techniques for isolation of these proteins, and have found that two of the surface proteins may be valuable vaccine candidates.

This work was presented at the NIH Symposium on Campylobacter jejuni at Asilomar, California and has been published in the Journal of Biological Chemistry (reprint attached).

The major points of the publication are that:

- 1. We have purified 4 different surface proteins migrating at 28 (PEB1), 29 (PEB2), 30 (PEB3), and (PEB4) kilodaltons.
- 2. All are highly basic proteins.
- 3. Most C. jejuni-infected persons but not controls sero-converted to PEB1 and PEB3.
- 4. Antiserum to PEB1 recognized all C. jejuni and C. coli strains but no other Campylobacter strains.

Therefore, the *C. jejuni* PEB1 and possibly PEB3 proteins appear to be candidate antigens for both a *Campylobacter* vaccine and for serologic assays for the pathogen.

5. Purification of a PEB1 analog in C. coli.

As reported above, we have purified a 28 kDa protein from C. jejuni that is commonly recognized by convalescent sera from C. jejuni—and C. coli—infected patients, and conserved in both species. We now purified a 28 kDa molecule from C. coli using cationic exchange FPLC. This molecule shares characteristics with the 28 kDa molecule of C. jejuni (PEB1-J) as follows: (i) Both are sensitive to proteinase K digestion, indicating that the major component is a protein. (ii) The two molecules have similar amino acid composition with basic amino acids predominating. (iii) The molecular weight of the C. coli protein is 28 kDa under non-denaturing conditions. The N-termini of the C. coli PEB1-C and C. jejuni proteins share 14 identical and 6 conserved amino acid residues in the first 20 residues, suggesting

that quantitative differences between *C. jejuni* and *C. coli* cells as determined by immunological assays may be due to antigenic differences. The N-terminus of the *C. coli* protein shared significant sequence homology with stress (heat-shock) proteins including *E. coli uvrA*, *E. coli* ATP-dependent protease La (lon) and *Bacillus megaterium* major heat shock protein (dnak). These data suggest that the conserved low molecular weight proteins of *C. jejuni* and *C. coli* may represent stress proteins, explaining their antigenic characteristics.

6. Studies of serologic response to Campylobacter jejuni lipopolysaccharides.

studied the serological response to lipopolysaccharide from four Campylobacter strains in 34 adults with inflammatory enteritis in Denver, using an enzyme-linked immunosorbent assay (ELISA) for detection of IgA, IgG, and IgM. LPS was prepared by the hot phenol-water method and each preparation had <3% protein contamination. Two LPS preparations were of the same C. jejuni 0-group antigen (0:4 and 0:5) as were isolated from seven patients each, one preparation was from a nontypable O-group (O:NT) strain, and the other from O:1. Comparing acute and convalescent sera for the 22 Campylobacter-infected patients, mean optical density levels rose significantly in all three immunoglobulin classes to all 4 LPS preparations. There was no significant rise in any immunoglobulin class to any LPS preparation in the patients infected with other pathogens. Seroconversion in one or more injunoglobulin class to any LPS was found in 17 of 22 Campylobacter-infected versus none of seven non-Campylobacter-infected patients (p<.02). Significant responses to 0:4 and 0:5 LPS were seen in the seven patients each infected with homologous O-group Campylobacter strains and to a variable degree in the 15 patients infected with Campylobacter heterologous O-groups. Our results indicate that intestinal infection with Campylobacter induces a serologic response to homologous and heterologous O-group LPS; the heterologous response may be due to shared Campylobacter core LPS antigens. The data, in conjunction with our earlier volunteer studies indicate that there are conserved epitopes in the C. je juni LPS core that could have value for vaccine development.

7. Identification and purification of a heat shock protein from Campylobacter jejuni.

This work is a continuation of our efforts in screening surface proteins of *C. jejuni* for vaccine candidates. We purified a 36 kDa protein from the glycine extract of strain 81-176 (which is the same strain from which PEB1 to 4 were purified), by using preparative SDS-PAGE (Figure 1). The purified 36 kDa protein which we now call PEB5, was tested for its ability to induce antibody

response in humans during natural infection. By using Western blotting, 3 of 3 convalescent sera from C. jejuni-infected patients recognized this band. The amino terminus of this protein was sequenced up to 28 amino acid residues. Similar to PEB1 to 4, the mature 36 kDa protein did not start with methionine at its Nterminus, indicating that post-translational cleavage of a leader peptide probably occurs. The N-terminus of 36 kDa protein shared very significant homology with a number of heat shock proteins of the cpn60 chaperonin family (Figure 2), including GroEL protein of E. coli (75% identity), 57 kDa chlamydial hypersensitivity antigen (75%), 65 kDa antigen (cell wall protein A) of Mycobacterium tuberculosis, and M. leprae (66%) and mitochondrial protein pl precursor of human and Chinese hamster cells (64%), and rubisco subunit bindingprotein alpha subunit precursor of wheat (57%). The 36 kDa protein (PEB5) is a possible common antigen in C. je juni, and by analogy to other chaperonin proteins could play a role in the immunopathogenesis of infection.

8. Cloning PEB1 from Campylobacter je juni.

As reported previously, we have identified and purified four C. jejuni proteins, PEB1 to 4. Two of these proteins, PEB1 and PEB3 were recognized by a majority (80%) of convalescent sera from C. jejuni or C. coli-infected patients and appear to have potential as vaccine candidates. In the last report we provided more evidence that PEB1 also was conserved in C. coli by purification and characterization of a PEB1-like protein from a C. coli strain. Based on this information, we have concentrated our efforts on cloning the gene for PEB1 in E. coli in order to develop a system for production of PEB1 in large quantities to meet the need for this antigen in vaccine trials in both animals and humans. accomplish this goal, genomic DNA was prepared from C. jejuni strain 81-176, and sheared by sonication. Fragments ranging from 1 to 10 kb were isolated using a Sepharose CL2B column, ligated to EcoRI linkers and inserted into the EcoRI site in lambda qtll. Recombinant phages were packaged and used to transform E. coli Y1088. The resulting bank was amplified in E. coli Y1090 cells and screened with polyclonal antibody to PEB1 protein from a rabbit Two positive recombinant plaques were hyperimmunized with PEB1. selected, purified to clonality, and found to contain the same 2.6 kb insert from C. jejuni (Figure 3). The insert from clone 1 was subcloned into pUC19 to create pPB1. The resulting clones were mapped by a variety of restriction enzymes (Figure 4). deletion mutations, plasmids containing 1.6 kb inserts in both orientations were identified and called pPB119 and pPB219. We next used Western blotting to confirm the production of PEB1 in pPB119 and pPB219, and to characterize the size of the gene product. Both pPB119 and pPB219 produced proteins of 28 kDa recognized by the antiserum specific for PEB1. The proteins were produced in the absence of any induction, suggesting that the insert contained the necessary promoter for transcription of the full length PEB1 gene. We then generated a series of deletion mutants from pPB119 by using

both restriction enzymes based on the physical map shown in Figure 2 and unidirectional deletion by exonuclease III to localize the PEB1 gene. We found that the 1.2 kb fragment between EcoRI and NcoI sites still produced the full length PEB1 protein of 28 kDa. Since there is a lacZ promotor located upstream of the insert, we asked whether induction of transcription from this promoter could improve production of PEB1 in these recombinant E. coli. In the absence of the inducer (IPTG) for the lacZ promoter, both pPB119 and pPB219 were able to produce PEB1, suggesting the insert may contain an appropriate promoter for PEB1 in addition to its structural gene. When induced by IPTG, production of PEB1 was significantly increased in pPB119 but not in pPB219, as judged by Western blotting. These data indicate that transcription of the PEB1 gene is in same orientation as lacZ in pPB119, but is in the opposite orientation in pPB219. Our future plans for this work are: (i) to improve the production of PEB1 (ii) develop a method for large scale purification of PEB1 protein from pPB119, and (iii) to sequence the PEB1 gene.

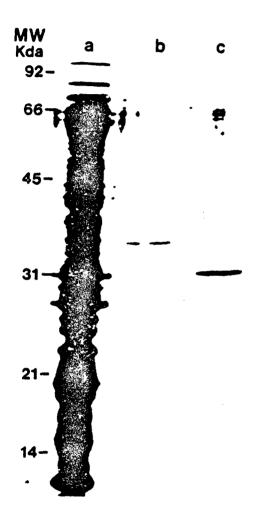


Figure 1 SDS-PAGE of PEB3 and PEB5 proteins purified from glycine extract of C. jejuni strain 81-176 using preparative SDS-PAGE. Lanes are: glycine extract (a); purified PEB5 (b); purified PEB3 (c); Protein bands were resolved by silver staining. Molecular weight markers are shown at left.

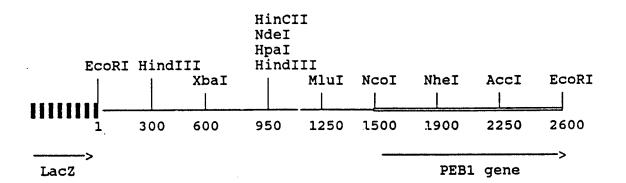


Figure 4. Physical map of C. jejuni insert in plasmid pFB1.

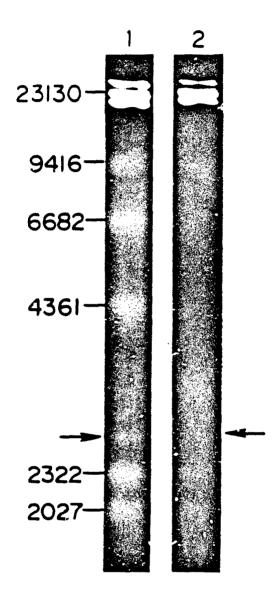


Figure 3 Agarose gel electrophoresis of phage DNA of two positive recombinants selected from lambda gtll gene bank. Lanes show EcoRI digestions of phage DNA from clone 1 (lane 1) and clone 2 (lane 2). The C. jejuni DNA inserts were released from the recombinant phage DNA after EcoRI digestion (as shown by arrows) and migrated with about 2600 base pairs. DNA molecular weight markers in base pairs are shown at left.

Identity with PEBS

PEB5 (36 KDa) of <u>C</u> . <u>jejuni</u>	(1) AANSDEKIGNLIADAMEKVGKDGVITVE (28)
Groel protein of <u>E</u> . <u>coli</u>	(150) SANSDETVGKLIAEAMOKVGKEGVITVE (177) 75%
57 KDa <u>Chlamydial</u> hypersensitivity antigen	(151) SANNDAEIGHLIAEAMEKVGKNGSITVE (178) 75%
65 KDa cell wall pprotein A of M. tuberculosis	(147) AAISAGDOSIGDLIAEAMOKVGNEGVITVE (176) 66%
65 KDa antigen of M. <u>leprae</u>	(147) AAISAGDOSIGDLIAEAMD <u>KVG</u> NEGVITVE (176) 66%
Mitochondial protein P1 of chinese Kamster and human	:: :::::::::::::::::::::::::::::::::::
Rubisco subunit binding-protein alpha subunit of wheat	: ::::::::::::::::::::::::::::::::::::
Putative 65 KDa chaperonin subunit of <u>Synechococcus</u> <u>sp</u>	(150) SÄGNÖFENÖGMÜNDÜNÖKNÖKEÖNISTE (177) 27%

Figure 2. Regional alignent of PEBS protein from <u>C. ieiuni</u> strain 81-176 with heat shock proteins of other sources. Conserved residues between PEBS and other heat proteins are indicated by ":". Residues conserved among all heat shock proteins are underlined. Number in parathesis represents position the sequence starts and ends at.

B. Publications:

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Blaser MJ, Olivares A, Taylor DN, Cornblath DR, McKhann GM. Campylobacter serology in patients with Chinese paralytic syndrome. Lancet 1991; 338:308.

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